## 5 **CLAIMS**

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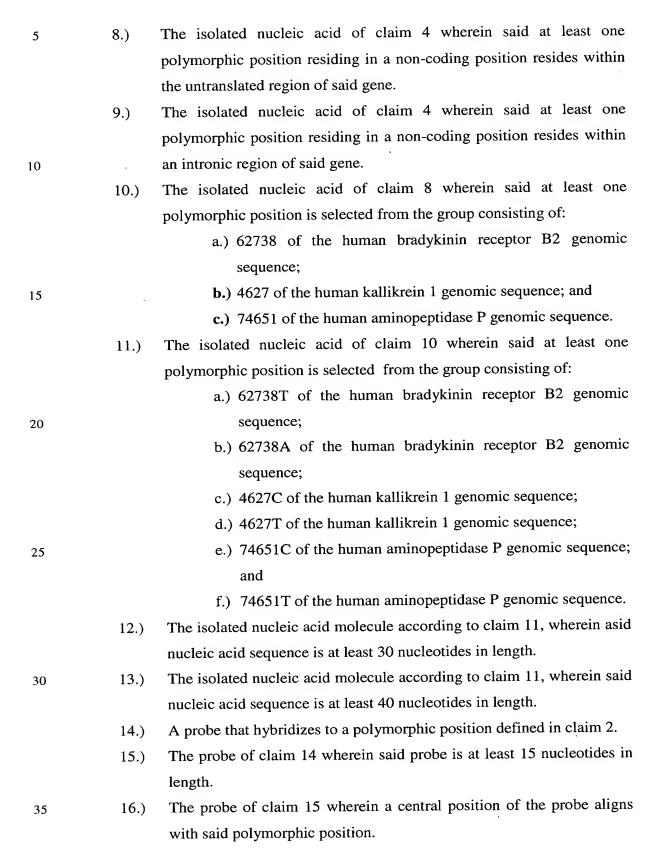
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## What is Claimed Is:

- 1.) An isolated nucleic acid derived from a human gene encoding a protein selected from a member of the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4), wherein said nucleic acid comprises at least one polymorphic position.
- The isolated nucleic acid of claim 1 wherein said at least one 2.) polymorphic position for each said gene is a polymorphic position specified in Table V, or complement thereof.
- The isolated nucleic acid of claim 2 wherein the sequence at said at 3.) least one polymorphic position is depicted in a nucleic acid sequence selected from the group consisting of SEQ ID NO: 163 to 288; 643 to 706; and 910 to 961, and 1574 to 1575, or complement thereof.
- 4.) The isolated nucleic acid of claim 3 wherein said at least one polymorphic position resides in a non-coding position within the genomic sequence of said gene.
- The isolated nucleic acid of claim 3 wherein said at least one 5.) polymorphic position resides in a coding position within the genomic sequence of said gene.
- 6.) The isolated nucleic acid of claim 5 wherein said at least one polymorphic position residing in a coding position results in a missense mutation of the translated product of said gene.
- 7.) The isolated nucleic acid of claim 5 wherein said at least one polymorphic position residing in a coding position results in a silent mutation of the translated product of said gene.



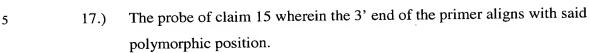
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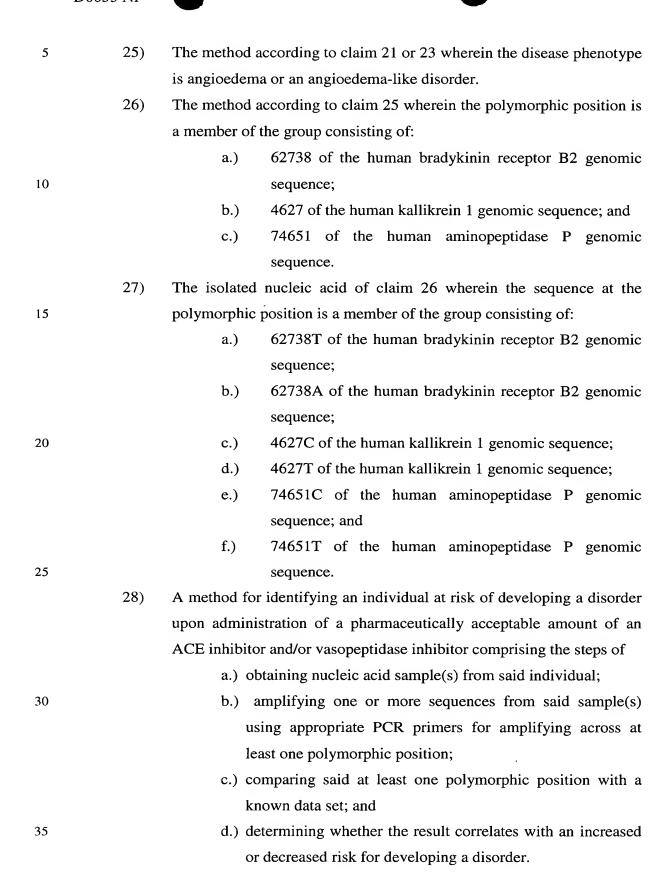
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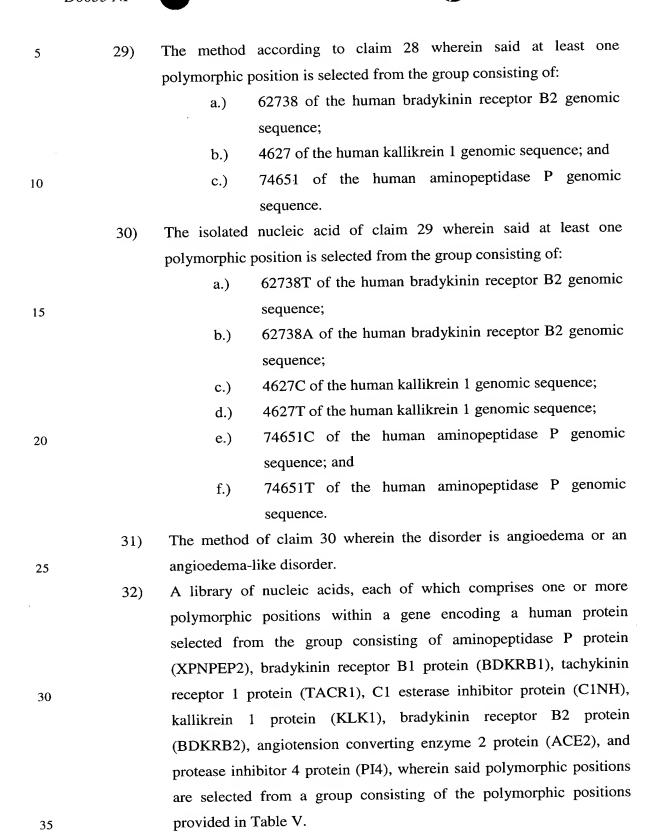
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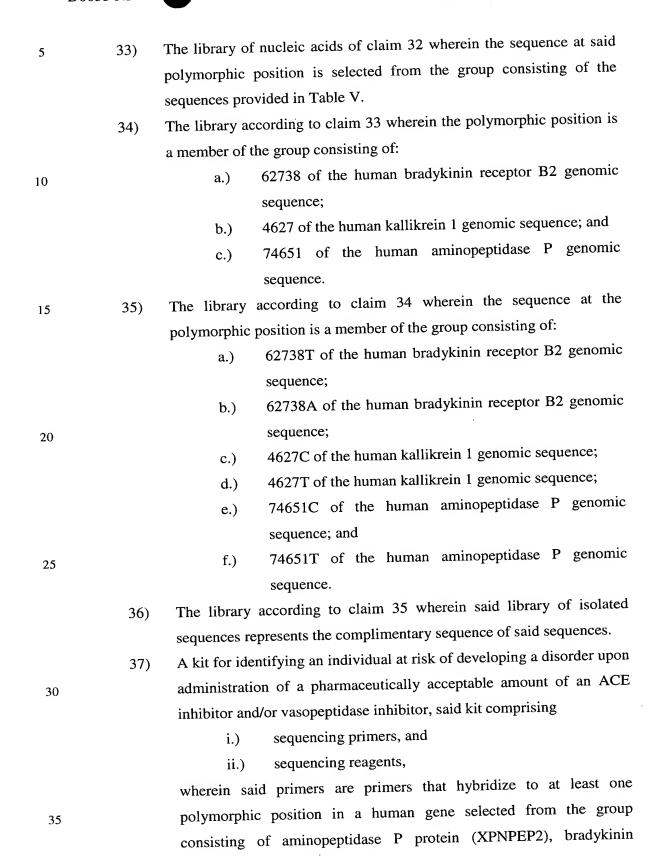
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- 18.) A method of analyzing at least one nucleic acid sample, comprising the steps of (1) obtaining said nucleic acid sample from one or more individuals; and (2) determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4).
- 19.) The method according to claim 18, further comprising the steps of (3) testing each individual for the presence of a disease phenotype; and (4) correlating the presence of the disease phenotype with the sequence at said one or more polymorphic positions.
- 20.) The method according to claim 19, wherein said one or more polymorphic position of said nucleic acid sequence is a polymorphic position specified in Table V for said gene.
- 21.) The method according to claim 20, wherein the nucleic acid sequence at said one or more polymorphic position is depicted in a nucleic acid sequence selected from the group consisting of SEQ ID NO:163 to 288; 643 to 706; and 910 to 961, and 1574 to 1575, or complement thereof.
- 22.) A method of constructing haplotypes using the isolated nucleic acids of claim 1, comprising the step of grouping at least two said nucleic acids.
- 23.) The method according to claim 22 further comprising the step of using said haplotypes to identify an individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with said haplotype.
- The method according to claim 19 further comprising the step of quantifying the nucleic acid sample comprising the polymorphic base.

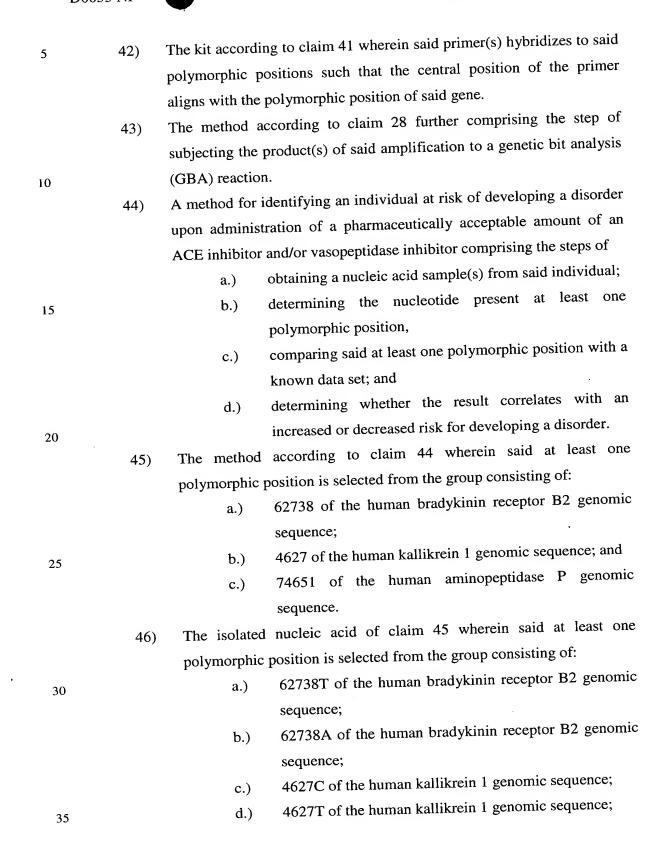






5		receptor B1 protein (BDKRB1), tachykinin receptor 1 protein
		(TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein
		(KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension
		converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein
		(PI4).
10	38)	The kit according to claim 37 wherein said polymorphic positions are
	,	selected from a group consisting of the polymorphic positions provided
		in Table V.
	39)	The kit according to claim 38 wherein the polymorphic position is a
	,	member of the group consisting of:
15		a.) 62738 of the human bradykinin receptor B2 genomic
		sequence;
		b.) 4627 of the human kallikrein 1 genomic sequence; and
		c.) 74651 of the human aminopeptidase P genomic
		sequence.
20	40)	The kit according to claim 39 wherein the sequence at the polymorphic
		position is a member of the group consisting of:
		a.) 62738T of the human bradykinin receptor B2 genomic
		sequence;
		b.) 62738A of the human bradykinin receptor B2 genomic
25		sequence;
		c.) 4627C of the human kallikrein 1 genomic sequence;
		d.) 4627T of the human kallikrein 1 genomic sequence;
		e.) 74651C of the human aminopeptidase P genomic
		sequence; and
30		f.) 74651T of the human aminopeptidase P genomic
		sequence.
	41)	The kit according to claim 40 wherein said primer(s) hybridizes

immediately adjacent to said polymorphic positions.



5	e.) 74651C of the human aminopeptidase P genomic
	sequence; and
	f.) 74651T of the human aminopeptidase P genomic
	sequence.
	47) The method of claim 46 wherein the disorder is angioedema or an
10	angioedema-like disorder.
	48) A method for genotyping an individual comprising the steps of
	a.) obtaining a nucleic acid sample(s) from said individual;
	b.) determining the nucleotide present at least one
	polymorphic position, and
15	c.) comparing said at least one polymorphic position with a
	known data set.
	49) The method according to claim 48 wherein said at least one
	polymorphic position is selected from the group consisting of:
	a.) 62738 of the human bradykinin receptor B2 genomic
20	sequence;
	b.) 4627 of the human kallikrein 1 genomic sequence; and
	c.) 74651 of the human aminopeptidase P genomic
	sequence.
	50) The isolated nucleic acid of claim 49 wherein said at least one
25	polymorphic position is selected from the group consisting of:
	a.) 62738T of the human bradykinin receptor B2 genomic
	sequence;
	b.) 62738A of the human bradykinin receptor B2 genomic
	sequence;
30	c.) 4627C of the human kallikrein 1 genomic sequence;
	d.) 4627T of the human kallikrein 1 genomic sequence;
	e.) 74651C of the human aminopeptidase P genomic
	sequence; and
	f.) 74651T of the human aminopeptidase P genomic
35	sequence.